



Sequences producing significant alignments:			Score (bits)	E Value	
<a href="#">gi 37182518 gb AAQ89061.1 </a>	TAAV688 [Homo sapiens]		<a href="#">451</a>	e-125	
<a href="#">gi 18088649 gb AAH20905.1 </a>	Presenilin stabilization factor-...		<a href="#">449</a>	e-125	<a href="#">L</a>
<a href="#">gi 13775224 ref NP_112591.1 </a>	presenilin stabilization facto...		<a href="#">447</a>	e-124	<a href="#">L</a>
<a href="#">gi 29243936 ref NP_808251.1 </a>	hypothetical protein 4632417K0...		<a href="#">391</a>	e-107	<a href="#">L</a>
<a href="#">gi 34864291 ref XP_217185.2 </a>	similar to RIKEN cDNA 0610008A...		<a href="#">377</a>	e-103	<a href="#">L</a>
<a href="#">gi 21492616 ref NP_080950.1 </a>	RIKEN cDNA 0610008A10 [Mus mus...		<a href="#">369</a>	e-101	<a href="#">L</a>
<a href="#">gi 41056229 ref NP_956409.1 </a>	anterior pharynx defective 1B ...		<a href="#">284</a>	2e-75	<a href="#">L</a>
<a href="#">gi 34864287 ref XP_343418.1 </a>	similar to RIKEN cDNA 0610008A...		<a href="#">282</a>	6e-75	<a href="#">L</a>
<a href="#">gi 14250557 gb AAH08732.1 </a>	APH-1A protein [Homo sapiens] >g...		<a href="#">256</a>	6e-67	<a href="#">L</a>
<a href="#">gi 12654775 gb AAH01230.1 </a>	APH-1A protein [Homo sapiens]		<a href="#">254</a>	1e-66	<a href="#">L</a>
<a href="#">gi 37077707 sp Q96BI3 AP1A HUMAN</a>	Gamma-secretase subunit AP...		<a href="#">254</a>	1e-66	<a href="#">L</a>
<a href="#">gi 22203751 ref NP_666216.1 </a>	anterior pharynx defective 1A ...		<a href="#">252</a>	7e-66	<a href="#">L</a>
<a href="#">gi 34858248 ref XP_345252.1 </a>	similar to Aphla-pending prote...		<a href="#">252</a>	9e-66	<a href="#">L</a>
<a href="#">gi 37077149 sp Q8BVF7 AP1A MOUSE</a>	Gamma-secretase subunit AP...		<a href="#">251</a>	2e-65	<a href="#">L</a>
<a href="#">gi 7705787 ref NP_057106.1 </a>	CGI-78 protein [Homo sapiens] >...		<a href="#">248</a>	2e-64	<a href="#">L</a>
<a href="#">gi 26324468 dbj BAC25988.1 </a>	unnamed protein product [Mus mu...		<a href="#">246</a>	5e-64	<a href="#">L</a>
<a href="#">gi 47214485 emb CAG12490.1 </a>	unnamed protein product [Tetrao...		<a href="#">211</a>	2e-53	
<a href="#">gi 48095709 ref XP_392345.1 </a>	similar to CG2855-PA [Apis mel...		<a href="#">178</a>	1e-43	<a href="#">L</a>
<a href="#">gi 20129183 ref NP_608710.1 </a>	CG2855-PA [Drosophila melanoga...		<a href="#">164</a>	2e-39	<a href="#">L</a>

<a href="#">gi 26347159 dbj BAC37228.1 </a>	unnamed protein product [Mus mu...	<u>162</u>	1e-38	<b>L</b>
<a href="#">gi 31233667 ref XP_318923.1 </a>	ENSANGP00000015809 [Anopheles ...	<u>158</u>	2e-37	
<a href="#">gi 39580694 emb CAE70374.1 </a>	Hypothetical protein CBG16933 [...	<u>81</u>	4e-14	
<a href="#">gi 17509423 ref NP_492469.1 </a>	i-78 protein like, Anterior PH...	<u>74</u>	6e-12	<b>L</b>
<a href="#">gi 18402667 ref NP_565724.1 </a>	expressed protein [Arabidopsis...	<u>70</u>	5e-11	
<a href="#">gi 21594204 gb AAM65980.1 </a>	unknown [Arabidopsis thaliana]	<u>69</u>	1e-10	
<a href="#">gi 20829201 ref XP_129583.1 </a>	similar to CGI-78 protein [Mus...	<u>62</u>	1e-08	
<a href="#">gi 22024126 ref NP_610786.2 </a>	CG8545-PA [Drosophila melanoga...	<u>36</u>	1.3	<b>L</b>
<a href="#">gi 32403290 ref XP_322258.1 </a>	hypothetical protein [Neurospo...	<u>35</u>	1.7	
<a href="#">gi 9837379 gb AAG00551.1 </a>	retinitis pigmentosa GTPase regul...	<u>35</u>	1.7	
<a href="#">gi 46309585 ref NP_908998.1 </a>	retrotransposon-like 1 [Mus mu...	<u>35</u>	2.2	<b>L</b>
<a href="#">gi 2209198 gb AAB61441.1 </a>	LOX6 [Helobdella robusta]	<u>35</u>	2.2	
<a href="#">gi 32414609 ref XP_327784.1 </a>	hypothetical protein [Neurospo...	<u>35</u>	2.9	
<a href="#">gi 41106711 ref XP_371313.1 </a>	similar to dJ14N1.2 (novel S-1...	<u>35</u>	2.9	<b>L</b>
<a href="#">gi 12314268 emb CAC13173.1 </a>	dJ14N1.2 (novel S-100/ICaBP typ...	<u>35</u>	2.9	
<a href="#">gi 32423411 ref XP_332143.1 </a>	predicted protein [Neurospora ...	<u>34</u>	3.8	
<a href="#">gi 46444603 gb EAL03877.1 </a>	hypothetical protein CaO19.1574 ...	<u>34</u>	5.0	
<a href="#">gi 46126293 ref XP_387700.1 </a>	hypothetical protein FG07524.1...	<u>34</u>	5.0	
<a href="#">gi 46444453 gb EAL03728.1 </a>	hypothetical protein CaO19.9147 ...	<u>34</u>	5.0	
<a href="#">gi 46228566 gb EAK89436.1 </a>	hypothetical protein with possib...	<u>34</u>	5.0	
<a href="#">gi 41054255 ref NP_956076.1 </a>	nuclear autoantigenic sperm pr...	<u>33</u>	6.5	<b>L</b>
<a href="#">gi 22328344 ref NP_680595.1 </a>	hypothetical protein [Arabidop...	<u>33</u>	6.5	
<a href="#">gi 465445 sp P33485 VNUA_PRVKA</a>	PROBABLE NUCLEAR ANTIGEN >gi...	<u>33</u>	6.5	
<a href="#">gi 9837383 gb AAG00553.1 </a>	retinitis pigmentosa GTPase regul...	<u>33</u>	8.5	
<a href="#">gi 6491868 gb AAF14051.1 </a>	myelin transcription factor 1-lik...	<u>33</u>	8.5	<b>L</b>
<a href="#">gi 7504867 pir  T23056</a>	hypothetical protein H06001.2 - Caen...	<u>33</u>	8.5	
<a href="#">gi 23508533 ref NP_701202.1 </a>	hypothetical protein [Plasmodi...	<u>33</u>	8.5	
<a href="#">gi 32563629 ref NP_491994.2 </a>	chromo domain and SNF2 related...	<u>33</u>	8.5	<b>L</b>
<a href="#">gi 42656368 ref XP_039762.5 </a>	myelin transcription factor 1-...	<u>33</u>	8.5	<b>L</b>
<a href="#">gi 38076711 ref XP_143396.2 </a>	similar to dJ14N1.2 (novel S-1...	<u>33</u>	8.5	<b>L</b>

## Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|37182518|gb|AAQ89061.1|](#) TAAV688 [Homo sapiens]  
Length = 257

Score = 451 bits (1159), Expect = e-125  
Identities = 230/257 (89%), Positives = 230/257 (89%)  
Frame = +3

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Query: 9  MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
          MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGA MARVII
Sbjct: 1  MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
           DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS
Sbjct: 61 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFFDG 548
           GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFFDG
Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFFDG 180

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Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKL 728  
 CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKL  
 Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779  
 CLLCQDKNFLLYNQRSR  
 Sbjct: 241 CLLCQDKNFLLYNQRSR 257

☐ >gi|18088649|gb|AAH20905.1| ☒ Presenilin stabilization factor-like [Homo sapiens]  
 Length = 257

Score = 449 bits (1154), Expect = e-125  
 Identities = 229/257 (89%), Positives = 229/257 (89%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 MTAAVFFGCAFIAGFPALALYVFTIA EPLRIIFLIAGA MARVII  
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368  
 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS  
 Sbjct: 61 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 548  
 GLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG  
 Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKL 728  
 CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKL  
 Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779  
 CLLCQDKNFLLYNQRSR  
 Sbjct: 241 CLLCQDKNFLLYNQRSR 257

☐ >gi|13775224|ref|NP\_112591.1| ☒ presenilin stabilization factor-like [Homo sapie  
 gi|37077447|sp|Q8WW43|AP1B\_HUMAN ☒ Gamma-secretase subunit APH-1B (APH-1b) (Aph-1  
 stabilization factor-like)  
 gi|12052866|emb|CAB66606.1| ☒ hypothetical protein [Homo sapiens]  
 gi|24637564|gb|AAN63817.1| ☒ presenilin stabilization factor-like protein [Homo s  
 Length = 257

Score = 447 bits (1150), Expect = e-124  
 Identities = 228/257 (88%), Positives = 229/257 (89%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 MTAAVFFGCAFIAGFPALALYVFTIA EPLRIIFLIAGA MARVII  
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368  
 DNKDGPTQKYLLIFGAFVSVYI+EMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS  
 Sbjct: 61 DNKDGPTQKYLLIFGAFVSVYIREMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDG 548  
 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDG  
 Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKL 728  
 CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKL  
 Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779  
 CLLCQDKNFLLYNQRSR  
 Sbjct: 241 CLLCQDKNFLLYNQRSR 257

☐ >[gi|29243936|ref|NP\\_808251.1|](#) ☒ hypothetical protein 4632417K02 [Mus musculus]  
[gi|37077156|sp|Q8C7N7|AP1B MOUSE](#) Gamma-secretase subunit APH-1B  
[gi|26340556|dbj|BAC33940.1|](#) ☒ unnamed protein product [Mus musculus]  
 Length = 257

Score = 391 bits (1004), Expect = e-107  
 Identities = 194/257 (75%), Positives = 210/257 (81%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXMARVII 188  
 MTAAVFFGCAFIAGFPALALYVFTIA +PLR+IFLIAGA + RVI  
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368  
 DN+DGP Q YLLIFG +SV IQE+FR AYYKLLKKASEGLKSINP ETAPSMRLLAYVS  
 Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYKLLKKASEGLKSINPEETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDG 548  
 GLGFGIMSGVFSFVNTLS+SLPGPTVGIHGDSPOFFL SAFMTLV+I+LHVFWG+VFFDG  
 Sbjct: 121 GLGFGIMSGVFSFVNTLSNSLPGPTVGIHGDSPOFFLNSAFMTLVVIMLHVFWGVVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKL 728  
 CEK KW S QTF+S YY +NL +A+II+VLMG WAF AGGSCRSCLKL  
 Sbjct: 181 CEKNKWYTLTLLTVLLTHLVSTQTFLLSPYEVNLTAYIIMVLMGIWAFYVAGGSCRSCLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779  
 CLLCQDK+FLLYNQRSR  
 Sbjct: 241 CLLCQDKDFLLYNQRSR 257

☐ >[gi|34864291|ref|XP\\_217185.2|](#) ☒ similar to RIKEN cDNA 0610008A10 [Rattus norvegi  
 Length = 257

Score = 377 bits (968), Expect = e-103  
 Identities = 189/257 (73%), Positives = 207/257 (80%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXMARVII 188  
 MTA VFFGCAFIAGFPALALY+FTIA +PLR+IFLIAGA + RVI  
 Sbjct: 1 MTAPVFFGCAFIAGFPALALYLFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368  
 DN+DGP Q YLLIFG +SV IQE+FR AYY+LLKKASEGLKSINP ETAPSMRLLAYVS

Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYRLKKASEGLKSINPEETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFDG 548  
GLGFGIMSGVFSFVNTLS++LPGPTVGIHGDSPQFFL SAFMTLVII+LHVFWGIVFFDG

Sbjct: 121 GLGFGIMSGVFSFVNTLSNALGPGPTVGIHGDSPQFFLNSAFMTLVIIMLHVFWGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLK 728  
CEK KW S QT +S +Y +NL +A+II+VLMG WAF AGGS RSLKL

Sbjct: 181 CEKNKWYILLTVLLTHLLVSTQTLLSPHYEVNLVTAYIIMVLMGIWAFVAGGSRRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779  
CLLCQDK+FLLYNQRSR

Sbjct: 241 CLLCQDKDFLLYNQRSR 257

☐ >gi|21492616|ref|NP\_080950.1| ☒ RIKEN cDNA 0610008A10 [Mus musculus]  
gi|37077773|sp|Q9DCZ9|AP1C MOUSE ☒ Putative gamma-secretase subunit APH-1C  
gi|12832198|dbj|BAB22004.1| ☒ unnamed protein product [Mus musculus]  
gi|29747906|gb|AAH50923.1| ☒ RIKEN cDNA 0610008A10 [Mus musculus]  
gi|38648719|gb|AAH63254.1| ☒ RIKEN cDNA 0610008A10 [Mus musculus]  
Length = 258

Score = 369 bits (948), Expect = e-101  
Identities = 186/258 (72%), Positives = 204/258 (79%), Gaps = 1/258 (0%)  
Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
MT VFFGCAFIAGFPA ALY+FTIA +PLR+IFLIAGA + RVI

Sbjct: 1 MTLPVFFGCAFIAGFPALALYFTIATDPLRVIFLIAGAFFWLVSLLSSMFVFLVRVIT 60

Query: 189 DNKDGPQTQYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGET-APSMRLLAYV 365  
+N+D Q YLLIFGA +SV IQE+FR AYYKLLKKASEGLKSINP E APSMRLLAYV

Sbjct: 61 NNRDESQNYLLIFGALLSVCIQELFRLAYYKLLKKASEGLKSINPEEDIAPSMRLLAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFD 545  
SGLGFGIMSGVFSFVNTLS+SLGPGPTVGIHGDSPQFFL SAFMTLV+I+LHVFWG+VFFD

Sbjct: 121 SGLGFGIMSGVFSFVNTLSNSLPGPTVGIHGDSPQFFLNSAFMTLVVIMLHVFWGVFFD 180

Query: 546 GCEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLK 725  
GCEK KW S QTF+S YY +NL +A+II+VLMG WAF AGGSCRSCLK

Sbjct: 181 GCEKNKWYLLTVLLTHLVVSTQTFSPYYEVNLVTAYIIMVLMGIWAFYVAGGSCRSCLK 240

Query: 726 LCLLCQDKNFLLYNQRSR 779  
CLLCQDK+FLLYNQRSR

Sbjct: 241 FCLLCQDKDFLLYNQRSR 258

☐ >gi|41056229|ref|NP\_956409.1| ☒ anterior pharynx defective 1B [Danio rerio]  
gi|37077309|sp|Q8JHE9|AP1B\_BRARE Gamma-secretase subunit Aph-1b (Anterior-pharynx  
1b)  
gi|22001127|gb|AAM88325.1| ☒ Aph-1 protein [Danio rerio]  
gi|37682171|gb|AAQ98012.1| ☒ anterior pharynx defective 1B-like [Danio rerio]  
gi|47939453|gb|AAH71492.1| ☒ Anterior pharynx defective 1B [Danio rerio]  
Length = 258

Score = 284 bits (726), Expect = 2e-75  
 Identities = 147/259 (56%), Positives = 183/259 (70%), Gaps = 2/259 (0%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 MT AVFFGC FIAFGPA+AL++FTIA +PLR+IFLIAGA + V I  
 Sbjct: 1 MTVAVFFGCTFIAFGPAIALFMFTIARDPLRVIFLIAGAFFWLVSLLLSSLVWFIT-VQI 59

Query: 189 DNKDGPTQKY-LLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLAY 362  
 NK+ TQ+ LLIFG +SV +QE FR+ YY+LLKKA+EGL +++ +T P SMR LAY  
 Sbjct: 60 SNKNSATQQRGLLIFGVVLSVLLQEAFFRYGYRLLKKANEGLLALSQEDTMPISMRQLAY 119

Query: 363 VSGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFF 542  
 VSGLGFG MSG FS VN LSDSLPGPTVGIHG+S +F+ SAFMTL IILLH+FWG+VFF  
 Sbjct: 120 VSGLGFGMSGAFSVVNILSDSLPGPTVGIHGESQHYFISSAFMTLAIILLHMFVGIVFF 179

Query: 543 DGCEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSL 722  
 + CE+++W S TF++ +Y +L +IIL +M WA+L AGGS R+L  
 Sbjct: 180 EACERQRWWALGAVVASHLVVSCLTFTVNPYQGS LIPTYIILSVMAVWAYLCAGGSLRNL 239

Query: 723 KLCLLCQDKNFLLYNQRSR 779  
 KLCL C+DK+FLL N R R  
 Sbjct: 240 KLCLTCKDKDFLLANHRPR 258

☐ >gi|34864287|ref|XP\_343418.1| ☒ similar to RIKEN cDNA 0610008A10 [Rattus norvegi]  
 Length = 216

Score = 282 bits (722), Expect = 6e-75  
 Identities = 151/257 (58%), Positives = 168/257 (65%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 MTAAVFFGCAFIAGFPAL+LYVFTIA +PLR+IFLIAGA + RVI  
 Sbjct: 1 MTAAVFFGCAFIAGFPALSLYVFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 368  
 DN+DGP Q YLLIFG +SV IQE+FR AYY+LLKKA+EGLKSINP ETAPSMRLAY  
 Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKANEGLKSINPEETAPSMRLAY-- 118

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFFDG 548  
 AFMTLVII+LHVFVGIVFFDG  
 Sbjct: 119 -----AFMTLVIIIMLHVFVGIVFFDG 139

Query: 549 CEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728  
 CEK KW S QT +S +Y +NL +A+II+VLMG WAF AGGS RSLKL  
 Sbjct: 140 CEKNKWYILLTVLLTHLLVSTQTLSPHYEVNLVTAYIIMVLMGIWAFCVAGGSRRSLKL 199

Query: 729 CLLCQDKNFLLYNQRSR 779  
 CLLCQDK+FLLYNQRSR  
 Sbjct: 200 CLLCQDKDFLLYNQRSR 216

☐ >gi|14250557|gb|AAH08732.1| ☒ APH-1A protein [Homo sapiens]  
☐ gi|14550502|gb|AAH09501.1| ☒ APH-1A protein [Homo sapiens]  
☐ gi|17389295|gb|AAH17699.1| ☒ APH-1A protein [Homo sapiens]

gi|22761292|dbj|BAC11529.1| **L** unnamed protein product [Homo sapiens]  
gi|25989508|gb|AAM61955.1| **L** presenilin stabilization factor a [Homo sapiens]  
gi|37183020|gb|AAQ89310.1| **L** GAAV579 [Homo sapiens]  
 Length = 247

Score = 256 bits (653), Expect = 6e-67  
 Identities = 129/247 (52%), Positives = 166/247 (67%), Gaps = 1/247 (0%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 M AAVFFGC F+AFGPA AL++ T+A +PLR+I L+AGA + +  
 Sbjct: 1 MGA AVFFGCTFVAFGPAFALFLITVAGDPLRVII LVAGAFFWLVSLLLASVWVFILVHVT 60

Query: 189 DNKDGPTQKYLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLAYV 365  
 D D Q LLIFGA VSV +QE+FRFAYYKLLKKA EGL S++ +P S+R +AYV  
 Sbjct: 61 DRSDARLQYGLLIFGA AVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFD 545  
 SGL FGI+SGVFS +N L+D+LGPG VGIHGDSP +FL SAF+T IILLH FWG+VFFD  
 Sbjct: 121 SGLSFGIISGVFSVINILADALGPGVVG I HGDSPYYFLTSAFLTAAIILLHTFWGVVFFD 180

Query: 546 GCEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAF LAAGGSCRS LK 725  
 CE++++ S TF++ +Y +L + + V MG WAF+ AGGS RS++  
 Sbjct: 181 ACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQ 240

Query: 726 LCLLCQD 746  
 LLC+D  
 Sbjct: 241 RSL LCKD 247

**L** >gi|12654775|gb|AAH01230.1| **L** APH-1A protein [Homo sapiens]  
 Length = 265

Score = 254 bits (650), Expect = 1e-66  
 Identities = 130/257 (50%), Positives = 170/257 (66%), Gaps = 4/257 (1%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 M AAVFFGC F+AFGPA AL++ T+A +PLR+I L+AGA + +  
 Sbjct: 1 MGA AVFFGCTFVAFGPAFALFLITVAGDPLRVII LVAGAFFWLVSLLLASVWVFILVHVT 60

Query: 189 DNKDGPTQKYLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLAYV 365  
 D D Q LLIFGA VSV +QE+FRFAYYKLLKKA EGL S++ +P S+R +AYV  
 Sbjct: 61 DRSDARLQYGLLIFGA AVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFD 545  
 SGL FGI+SGVFS +N L+D+LGPG VGIHGDSP +FL SAF+T IILLH FWG+VFFD  
 Sbjct: 121 SGLSFGIISGVFSVINILADALGPGVVG I HGDSPYYFLTSAFLTAAIILLHTFWGVVFFD 180

Query: 546 GCEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAF LAAGGSCRS LK 725  
 CE++++ S TF++ +Y +L + + V MG WAF+ AGGS RS++  
 Sbjct: 181 ACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSIRSIQ 240

Query: 726 LCLLC---QDKNFLLYN 767  
 LLC +D ++Y+  
 Sbjct: 241 RSL LCRREQEDSRVMVYS 257

☐ >[gi|37077707|sp|Q96BI3|APH1A HUMAN](#) ☒ Gamma-secretase subunit APH-1A (APH-1a) (Aph stabilization factor) (CGI-78) (UNQ579/PRO1141)

[gi|15990414|gb|AAH15568.1|](#) ☒ APH-1A protein [Homo sapiens]

[gi|18088501|gb|AAH20590.1|](#) ☒ APH-1A protein [Homo sapiens]

[gi|25989510|gb|AAM61956.1|](#) presenilin stabilization factor b [Homo sapiens]

Length = 265

Score = 254 bits (650), Expect = 1e-66

Identities = 130/257 (50%), Positives = 170/257 (66%), Gaps = 4/257 (1%)

Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
M AAVFFGC F+AFGPA AL++ T+A +PLR+I L+AGA + +

Sbjct: 1 MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVFILVHVT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLAYV 365  
D D Q LLIFGA VSV +QE+FRFAYYKLLKKA EGL S++ +P S+R +AYV

Sbjct: 61 DRSDARLQYGLLIFGA AVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYV 120

Query: 366 SGLGFGIMSGVFSFVNLTSLGPGTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFD 545  
SGL FGI+SGVFS +N L+D+LGPG VGIHGDSP +FL SAF+T IILLH FWG+VFFD

Sbjct: 121 SGLSFGIISGVFSVINILADALGPGVVGVIHGDSPYYFLTSAFLTAAIILLHTFWGVVFFD 180

Query: 546 GCEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLK 725  
CE++++ S TF++ +Y +L + + V MG WAF+ AGGS RS++

Sbjct: 181 ACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQ 240

Query: 726 LCLLC---QDKNFLLYN 767  
LLC +D ++Y+

Sbjct: 241 RSLLCRRQEDSRVMVYS 257

☐ >[gi|22203751|ref|NP\\_666216.1|](#) ☒ anterior pharynx defective 1A homolog; anterior 1A homolog (C. elegans) [Mus musculus]

[gi|15341753|gb|AAH12406.1|](#) ☒ Anterior pharynx defective 1A homolog [Mus musculus]

[gi|34786036|gb|AAH57865.1|](#) ☒ Anterior pharynx defective 1A homolog [Mus musculus]

Length = 247

Score = 252 bits (644), Expect = 7e-66

Identities = 127/247 (51%), Positives = 165/247 (66%), Gaps = 1/247 (0%)

Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
M AAVFFGC F+AFGPA +L++ T+A +PLR+I L+AGA + +

Sbjct: 1 MGAAVFFGCTFVAFGPAFSLFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVFILVHVT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLAYV 365  
D D Q LLIFGA VSV +QE+FRFAYYKLLKKA EGL S++ +P S+R +AYV

Sbjct: 61 DRSDARLQYGLLIFGA AVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYV 120

Query: 366 SGLGFGIMSGVFSFVNLTSLGPGTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFD 545  
SGL FGI+SGVFS +N L+D+LGPG VGIHGDSP +FL SAF+T IILLH FWG+VFFD

Sbjct: 121 SGLSFGIISGVFSVINILADALGPGVVGVIHGDSPYYFLTSAFLTAAIILLHTFWGVVFFD 180

Query: 546 GCEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLK 725  
CE++++ S TF++ +Y +L + + V MG WAF+ AGGS RS++



Sbjct: 181 ACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQ 240

Query: 726 LCLLCQD 746

L C+D

Sbjct: 241 RSLSCKD 247

☐ >gi|34858248|ref|XP\_345252.1| ☒ similar to Aphla-pending protein [Rattus norvegi  
Length = 265

Score = 252 bits (643), Expect = 9e-66

Identities = 129/257 (50%), Positives = 169/257 (65%), Gaps = 4/257 (1%)

Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
M AAVFFGC F+AFGPA AL++ T+A +PLR+I L+AGA + +

Sbjct: 1 MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVFILVHVT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLLAYV 365  
D D Q LLIFGA VSV +QE+FRFAYYKLLKKA EGL S++ +P S+R +AYV

Sbjct: 61 DRSDARLQYGLLIFGAASVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFD 545  
SGL FGI+SGVFS +N L+D+LGPG VGIHGDSP +FL SAF+T IILLH FWG+VFFD

Sbjct: 121 SGLSFGIISGVFSVINILADALGPGVVGIIHGDSPYYFLTSAFLTAAIILLHTFWGVVFFD 180

Query: 546 GCEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLK 725  
CE++++ S TF++ +Y +L + + V MG WAF+ AGGS RS++

Sbjct: 181 ACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFVITAGGSLRSIQ 240

Query: 726 LCLLC---QDKNFLLYN 767

L C +D ++Y+

Sbjct: 241 RSLSCRRQEDSRVMVYS 257

☐ >gi|37077149|sp|Q8BVF7|AP1A-MOUSE ☒ Gamma-secretase subunit APH-1A  
gi|18848275|gb|AAH24111.1| ☒ 6530402N02Rik protein [Mus musculus]  
Length = 265

Score = 251 bits (641), Expect = 2e-65

Identities = 128/257 (49%), Positives = 169/257 (65%), Gaps = 4/257 (1%)

Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
M AAVFFGC F+AFGPA +L++ T+A +PLR+I L+AGA + +

Sbjct: 1 MGAAVFFGCTFVAFGPAFSLFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVFILVHVT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLLAYV 365  
D D Q LLIFGA VSV +QE+FRFAYYKLLKKA EGL S++ +P S+R +AYV

Sbjct: 61 DRSDARLQYGLLIFGAASVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFD 545  
SGL FGI+SGVFS +N L+D+LGPG VGIHGDSP +FL SAF+T IILLH FWG+VFFD

Sbjct: 121 SGLSFGIISGVFSVINILADALGPGVVGIIHGDSPYYFLTSAFLTAAIILLHTFWGVVFFD 180

Query: 546 GCEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLK 725  
CE++++ S TF++ +Y +L + + V MG WAF+ AGGS RS++

Sbjct: 181 ACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQ 240

Query: 726 LCLLC---QDKNFLLYN 767

L C +D ++Y+

Sbjct: 241 RSLSCRRQEDSRVMVYS 257

☐ >[gi|7705787|ref|NP\\_057106.1|](#) ☒ CGI-78 protein [Homo sapiens]  
[gi|4929623|gb|AAD34072.1|](#) ☒ CGI-78 protein [Homo sapiens]  
[gi|24637562|gb|AAN63816.1|](#) ☒ presenilin stabilization factor [Homo sapiens]  
 Length = 251

Score = 248 bits (632), Expect = 2e-64

Identities = 125/240 (52%), Positives = 161/240 (67%), Gaps = 1/240 (0%)

Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 M AAVFFGC F+AFGPA AL++ T+A +PLR+I L+AGA + +

Sbjct: 1 MGA AVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVT 60

Query: 189 DNKDGPTQKYLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLLAYV 365  
 D D Q LLIFGA VSV +QE+FRFAYYKLLKKA EGL S++ +P S+R +AYV

Sbjct: 61 DRSDARLQYGLLIFGA AVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFWGVFFD 545  
 SGL FGI+SGVFS +N L+D+LGPG VGIHGDSP +FL SAF+T IILLH FWG+VFFD

Sbjct: 121 SGLSFGIISGVFSVINILADALPGVVGIVHGDSPYYFLTSAFLTAAIILLHTFWGVVFFD 180

Query: 546 GCEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSRK 725  
 CE+++ S TF++ +Y +L + + V MG WAF+ AGGS RS++

Sbjct: 181 ACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQ 240

☐ >[gi|26324468|dbj|BAC25988.1|](#) ☒ unnamed protein product [Mus musculus]  
 Length = 212

Score = 246 bits (628), Expect = 5e-64

Identities = 126/159 (79%), Positives = 133/159 (83%)

Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 MTA AVFFGCAFIAGFPALALYVFTIA +PLR+IFLIAGA + RVI

Sbjct: 1 MTA AVFFGCAFIAGFPALALYVFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPTQKYLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368  
 DN+DGP Q YLLIFG +SV IQE+FR AYYKLLKKASEGLKSINP ETAPSMRLLAYVS

Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYKLLKKASEGLKSINPEETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYS 485  
 GLGFGIMSGVFSFVNTLS+SLPGPTVGIHGDSPQFFL S

Sbjct: 121 GLGFGIMSGVFSFVNTLSNSLPGPTVGIHGDSPQFFLNS 159

☐ >[gi|47214485|emb|CAG12490.1|](#) unnamed protein product [Tetraodon nigroviridis]  
 Length = 217

Score = 211 bits (536), Expect = 2e-53  
 Identities = 120/258 (46%), Positives = 145/258 (56%), Gaps = 1/258 (0%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 MTAAVFFGC FIAFGPA++L+VFTIA EPLR+IFLIAGA ++ I  
 Sbjct: 1 MTAAVFFGCTFIAFGPAISLFVFTIAREPLRVIFLIAGAFFWLVSLLLSSLVWFISVQIS 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLAYV 365  
 D QK LLIFG +SV +QE FRFAYYKLLKKA+EGL +++ ET P S R LAY  
 Sbjct: 61 DKDSAAQQKGLLIFGVVLSVVLQETFRFAYYKLLKKANEGLTLSQEETMPISTRQLAY- 119

Query: 366 SGLGFGIMSGVFSFVNTLSDSLPGTGVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFD 545  
 AFMT+ IILLH+FWG+VFFD  
 Sbjct: 120 -----AFMTMAIILLHMFHWGVVFFD 139

Query: 546 GCEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLK 725  
 CEK++W S TF + Y +L +++L LMG WAF AGGS R+LK  
 Sbjct: 140 ACEKQRWVAVAVVISHLIVSCLTFQNPYSVASLVPTYVVLFLMGIWAFYTAGGSLRNLK 199

Query: 726 LCLLCQDKNFFLYNQSR 779  
 LCL C+DK+ LL N RSR  
 Sbjct: 200 LCLTCKDKDLLLANHRSR 217

☐ >[gi|48095709|ref|XP\\_392345.1|](#) ☒ similar to CG2855-PA [*Apis mellifera*]  
 Length = 238

Score = 178 bits (452), Expect = 1e-43  
 Identities = 101/243 (41%), Positives = 131/243 (53%), Gaps = 2/243 (0%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 MT FFGCAF+AFGP LA++ FT+A EP+RII LIA A I+  
 Sbjct: 1 MTVMDFFGCAFLAFGPPLAMFTFTVAAEPIRIIILIASAFFWLISLLLSS-----IL 52

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 368  
 P Q +L FG SV QE FR+ Y +L+KA GL + A S + AYV  
 Sbjct: 53 WYAVVPLQNHLA-FGLVFSVLFQEAFFRYLLYWVLRKAERGLDKVTTHVADSRHVFAYVC 111

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGTGVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFDG 548  
 GLGFG MSGVF+ VN L+D++GPGT+G+ + FF+ SA TL ILLH FWG+VFF  
 Sbjct: 112 GLGFGMSGVFALNVLADAVGPGTMGLRQGEYFFVISAATTLCFILLHTFWGVVFFSA 171

Query: 549 CEKKKWGXXXXXXXXXXXXSAQTF--ISSYYGINLASAFIILVLMGTWAFLAAGGSCRSL 722  
 ++K WG S T + Y SA++IL++ AF AGG +S+  
 Sbjct: 172 LDRKNWGQVIWVGSHLFVSCMTLLNVKEAYVATTL SAYVILMITTALAFKVAGGRPQSI 231

Query: 723 KLC 731  
 C  
 Sbjct: 232 VQC 234

☐ >[gi|20129183|ref|NP\\_608710.1|](#) ☒ CG2855-PA [*Drosophila melanogaster*]  
[gi|37077998|sp|Q9VQG2|APH1\\_DROME](#) Gamma-secretase subunit Aph-1 (Presenilin stabil  
[gi|7295913|qb|AAF51212.1|](#) ☒ CG2855-PA [*Drosophila melanogaster*]

gi|15291627|gb|AAK93082.1| **L** LD12037p [Drosophila melanogaster]  
gi|24637560|gb|AAN63815.1| presenilin stabilization factor [Drosophila melanogaster]  
 Length = 238

Score = 164 bits (415), Expect = 2e-39  
 Identities = 94/248 (37%), Positives = 131/248 (52%), Gaps = 3/248 (1%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 MT FFGC FIAFGP AL+VFTIA +P+RII LIA A + +  
 Sbjct: 1 MTLPEFFGCTFIAFGPPFALFVFTIANDPVRIIILIAAAFFWLLSLLISSLWYALIPL-- 58

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSI-NPGETAPSMRLLAYV 365  
 K L FG SV QE FR+ Y++L+ +GL ++ + +LAYV  
 Sbjct: 59 -----KEFLAFGVVFSVCFQEAFLRYIIYRILRSTEQGLHAVAEDTRVTDNKHILAYV 110

Query: 366 SGLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPPQFFLYSAFMTLVIILLHVFHWGIVFFD 545  
 SGLGFGI+SG+F+ VN L+D GPGT+G+ G + FF+ SA L IILLH FW ++FF+  
 Sbjct: 111 SGLGFGIISGMFALVNVLADMSGPGTMGLKGGTELFVTSAAQALSIIILLHTFWSVIFFN 170

Query: 546 GCEKKKWGXXXXXXXXXXXXXSAQTFISS--YYGINLASAFIILVLMGTWAFLAAGGSCRS 719  
 + + S T +++ Y L +++ +L G AF AGG+ RS  
 Sbjct: 171 AFDTNNYIHIGYVVFSLFVSLITLLNANELYTTTLLINYLVTILTGVLAFRVAGGTSRS 230

Query: 720 LKLCLLCQ 743  
 + + CQ  
 Sbjct: 231 FRKFITCQ 238

gi|26347159|dbj|BAC37228.1| **L** unnamed protein product [Mus musculus]  
 Length = 152

Score = 162 bits (409), Expect = 1e-38  
 Identities = 78/152 (51%), Positives = 104/152 (68%), Gaps = 1/152 (0%)  
 Frame = +3

Query: 294 KASEGLKSINPGETAP-SMRLLAYVSGLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPPQ 470  
 KA EGL S++ +P S+R +AYVSGL FGI+SGVFS +N L+D+LGPG VGIHGDS  
 Sbjct: 1 KADEGLASLEDGRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIVHGDSFY 60

Query: 471 FFLYSAFMTLVIILLHVFHWGIVFFDCEKWKWXXXXXXXXXXXXXSAQTFISSYYGINLA 650  
 +FL SAF+T IILLH FWG+VFFD CE++++ S TF++ +Y +L  
 Sbjct: 61 YFLTSAFLTAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLL 120

Query: 651 SAFIILVLMGTWAFLAAGGSCRSCLKLCLLCQD 746  
 + + V MG WAF+ AGGS RS++ L C+D  
 Sbjct: 121 PIYAVTVSMGLWAFITAGGSLRSIQRSLSCKD 152

gi|31233667|ref|XP\_318923.1| ENSANGP00000015809 [Anopheles gambiae]  
gi|30174614|gb|EAA14158.2| ENSANGP00000015809 [Anopheles gambiae str. PEST]  
 Length = 247

Score = 158 bits (399), Expect = 2e-37  
 Identities = 93/250 (37%), Positives = 134/250 (53%), Gaps = 5/250 (2%)  
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 MT FFGC+F+AFGP +A++ TIA +P+RII LIA A +A +  
 Sbjct: 7 MTVVEFFGCSFLAFGPPVAMFALTIAHDPIRIIILIA-ASFFWLVSLLSSTVWLAHPV 65

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQ--EMFRFAYYKLLKKASEGLKSINP-GETAPSMRLLA 359  
 +K + FG SV+IQ + FR+ YK+L+K GL+ + A +L+  
 Sbjct: 66 TSK-----VTFGLICSVFIQVCKRFRYLMYKVLKTESGLQEVTDIVRIADYRHLS 117

Query: 360 YVSGLGFGIMSGVFSFVNTLSDSLPGTVGIHGDS PQFFLYSAFMTLVIILLHVFVGIVF 539  
 Y SGLGFGI+SG FS VN L+DS+GP TVG+ S F L SA +L +ILLH FW ++F  
 Sbjct: 118 YASGLGFGIISGAFSLVNILADSVGPATVGLKAASDIFMLISAAQSLAMILLHTFWSVIF 177

Query: 540 FDGCEKKKWGXXXXXXXXXXXXXSAQTFI--SSYYGINLASAFIILVLMGTWAFLAAGGSC 713  
 F+ C+ K + S T + S Y + L ++ ++ + G AF AGG+  
 Sbjct: 178 FNACDVKNYYHIGYVVASHLFVSCMTLLNASGLYAVTLLISYTMVCITGAIAFQVAGGTV 237

Query: 714 RSLKLCLLCQ 743  
 S + L C+  
 Sbjct: 238 ASFRKFLTCK 247

☐ >[gi|39580694|emb|CAE70374.1|](#) Hypothetical protein CBG16933 [Caenorhabditis briggs]  
 Length = 1387

Score = 80.9 bits (198), Expect = 4e-14  
 Identities = 61/209 (29%), Positives = 96/209 (45%), Gaps = 24/209 (11%)  
 Frame = +3

Query: 3 VAMTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARV 182  
 + M + C +F P++AL+ IA +P+RII G+  
 Sbjct: 1071 IKMGIVLTVSCYIASFSPSIALFYSFIAHDPVRIILFFLGSSFFWLVSLLISSLAWLGLST 1130

Query: 183 IIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLK-----SINPG--E 332  
 ++ N +L+ G V + QE+ R AY+ LLKKA +GL S+ PG +  
 Sbjct: 1131 VLPNT-----FLISLG--VCIVAQELSRVAYFMLLKKAKGLNKITRHGQISVAPGVSD 1182

Query: 333 TAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLPGTVGI-----HGDS-----PQ 470  
 + +LA V GLG G++S +F +N + GPGT+G+ H DS P  
 Sbjct: 1183 LHNARHMLALVCGLGMVISALFYTMNAFATFAGPGTIGLPMALLETGHIDSNRAGKYLPL 1242

Query: 471 FFLYSAFMTLVIILLHVFVGIVFFDGCEK 557  
 ++ SA +++ L HV W I+ +D C K  
 Sbjct: 1243 CYVLSA---ILLTLFHVAVTIMVWDTCHK 1268

☐ >[gi|17509423|ref|NP\\_492469.1|](#) ☒ i-78 protein like, Anterior PHarynx defective AP  
 Enhancer (enhancer of sel-12 null) PEN-1 (aph-1)  
 [Caenorhabditis elegans]  
[gi|37076812|sp|O45876|APH1 CAEEL](#) Gamma-secretase subunit aph-1 (Anterior-pharynx-  
 1) (Presenilin enhancer protein 1)  
[gi|17508722|pir||T26007](#) hypothetical protein VF36H2L.1 - Caenorhabditis elegans  
[gi|3880371|emb|CAA16282.1|](#) C. elegans APH-1 protein (corresponding sequence VF36H  
 [Caenorhabditis elegans]  
 Length = 308

Score = 73.6 bits (179), Expect = 6e-12  
 Identities = 63/257 (24%), Positives = 105/257 (40%), Gaps = 28/257 (10%)

Frame = +3

Query: 33 CAFIAFGPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVIIDNKDGPTQ 212  
 C +F P++AL+ IA +P+RII G+ ++ +  
 Sbjct: 9 CYIASFSPSIALFCSFIAHDPVRIILFFLGSSFFWLVSLLFSSLAWLGLSTVLPDT----- 63

Query: 213 KYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLK-----SINPG--ETAPSMRLLAY 362  
 + V + QE+ R AY+ LLKKA GL S+ PG + + +LA  
 Sbjct: 64 ---FLLSLTVCIIAQELSRVAYFMLLKKKAQRGLNKITRQQGISVAPGVSDLHNARHMLAL 120

Query: 363 VSGLGFGIMSGVFSFVNTLSDSLPGPTVGI-----HGDSPQFFLYSAFMTLVII 509  
 V GLG G++S +F +N + GPGT+G+ + L +++  
 Sbjct: 121 VCGLGMGVISALFYTMNAFAIFSGPGTIGLPNALKTGEIDTNRAGKYLPLCYTSLAILLT 180

Query: 510 LLHVFHWGIVFFDGCEK--KKWGXXXXXXXXXXXXXSAQTFISS-----YYGINLASAFIIL 668  
 L HV W I+ +D C K + TF+SS ++ + A F+IL  
 Sbjct: 181 LFHVTWTIMVWDSCHKIGRIPSAFVPGAAAVVSHLLVTFLSSLNSRFGHVLVFAVQFLIL 240

Query: 669 VLMGTWAFLAAGGSCRS 719  
 ++ + + GG+ S  
 Sbjct: 241 LICIAYCNVIMGGTISS 257

☐ >gi|18402667|ref|NP\_565724.1| expressed protein [Arabidopsis thaliana]  
 gi|37077331|sp|Q8L9G7|APH1 ARATH Gamma-secretase subunit APH1-like  
 gi|17381290|gb|AAL36063.1| At2g31440/T28P16.7 [Arabidopsis thaliana]  
 gi|20198156|gb|AAD26475.2| unknown protein [Arabidopsis thaliana]  
 gi|20453379|gb|AAM19928.1| At2g31440/T28P16.7 [Arabidopsis thaliana]  
 Length = 250

Score = 70.5 bits (171), Expect = 5e-11

Identities = 53/189 (28%), Positives = 86/189 (45%), Gaps = 6/189 (3%)

Frame = +3

Query: 9 MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188  
 MT A G A +A GP+L+L+V I+ +P I+ +++ + R +  
 Sbjct: 1 MTVAAGIGYALVALGPSLSLFSVVISRKPFLILTVLSSTLLWLVSLLIILSG---LWRPFL 57

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRL----- 353  
 K Y L+ SV QE RF ++K+ K+ + L S + P + L  
 Sbjct: 58 PLKANVWWPYALL--VITSVCFQEGRLFLFWKVYKRLDVDLDSFADRISRPRFLFLTDKLQ 115

Query: 354 LAYVSGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSP-QFFLYSAFMTLVIIILLHVFHWG 530  
 +A GLG G+ VF ++ L+ + GP T + S FFL SA + L + +H F  
 Sbjct: 116 IALAGGLGHGVAHAVFFCLSLTPAFGPATFYVERCSKVPFFLISAIIALAFVTIHTFSM 175

Query: 531 IVFFDGCEK 557  
 ++ F+G K  
 Sbjct: 176 VIAFEGYAK 184

☐ >gi|21594204|gb|AAM65980.1| unknown [Arabidopsis thaliana]  
 Length = 250

Score = 69.3 bits (168), Expect = 1e-10

Identities = 52/189 (27%), Positives = 86/189 (45%), Gaps = 6/189 (3%)

Frame = +3



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Protein

Genome

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PMC

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Preview/Index

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☐ 1: AAH20905. Presenilin stabil...[gi:18088649]

BLink, Domains, Links

LOCUS AAH20905 257 aa linear PRI 29-JUN-2004  
 DEFINITION Presenilin stabilization factor-like [Homo sapiens].  
 ACCESSION AAH20905  
 VERSION AAH20905.1 GI:18088649  
 DBSOURCE accession BC020905.1  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (residues 1 to 257)  
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,  
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,  
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,  
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,  
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,  
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,  
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,  
 Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,  
 Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S.,  
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,  
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,  
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,  
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,  
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
 TITLE Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 PUBMED 12477932  
 REFERENCE 2 (residues 1 to 257)  
 AUTHORS Strausberg,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: CLONTECH  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 37 Row: f Column: 15  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 13775223.  
Method: conceptual translation.

## FEATURES

## source

Location/Qualifiers

1..257

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="MGC:24164 IMAGE:4720647"

/tissue\_type="Placenta"

/clone\_lib="NIH\_MGC\_79"

/lab\_host="DH10B"

/note="Vector: pDNR-LIB"

Protein

1..257

/product="presenilin stabilization factor-like"

CDS

1..257

/gene="PSFL"

/coded\_by="BC020905.1:17..790"

/db\_xref="LocusID:83464"

/db\_xref="MIM:607630"

## ORIGIN

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121 glgfgimsgv fsfvntlsds lpggtvgihg dspqfflysa fmtlviillh vfwgivffdg
181 cekkkwgill ivllthllvs aqtfissyg inlasafiil vlmgtwafla aggsrslkl
241 cllcqdknfl lynqrslr
```

//

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Jun 8 2004 17:01:12